Deciphering phenotypic diversity of *Ralstonia solanacearum* strains pathogenic to potato

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Based on the phylotype classification scheme, we questioned how genetically and phenotypically diverse may strains of *Ralstonia solanacearum* pathogenic to potato are. We studied 129 representative European and Mediterranean strains of *R. solanacearum* along with 57 reference strains known to cover the genetic diversity in this species. Phylogeny analysis was done on partial endoglucanase (*egl*) gene sequences. Virulence and pathogenicity to potato, tomato, and eggplant was established at two ranges of temperature 24-30°C (tropical) and 15-24°C (temperate) and tests on banana were only conducted at 24-30°C.

Results confirm the literature that the ability to cause wilt on *Solanaceae* and specially on potato was of polyphyletic nature and shared by strains in all phylotypes I, IIA, IIB, III, and IV, showing a wide genetic basis for pathogenicity on these hosts. We also noticed that strains that were known to cause wilt on *Musaceae* solely: phylotypes IIA sequevar 6 (IIA-6), IIB-3, and IIB-4, were also able to trigger wilt on *Solanaceae*, especially on susceptible potato, tomato and eggplant, and also on some resistant tomato for the phylotype IIB-4. In the same time, we isolated Brown rot potato strains belonging to phylotypes IIB-1 and IIB-2, but also strains belonging to phylotype IIB-27, from symptomless banana plants, also suggesting the polyphyletic nature of the Moko disease-causing strains. That said, from an epidemiological point of view, no Moko disease causing strains have ever been isolated from a wilted tomato or potato in the field, although it is now apparent they were able to trigger wilt in these hosts. But from a phylogenetic point of view, these two well known ecotypes address the question of host adaptation mechanisms, which may have undergone a similar bottleneck evolution.

On the contrary, cold-tolerance ability on *Solanaceae* is only shared among the clonal brown rot phylotype IIB-1, which gathered the great majority of European and Mediterranean (EuMr) strains. All other strains were not able to trigger wilt or were drastically less aggressive on these hosts. A total of 5 strains out of 106 originating or intercepted in EuMr countries were not distributed into the phylotype IIB-1 and showed that despite the great proportion of brown rot phylotypes IIB-1 strains on EuMr territory, other phylotypes may represent a potential threat to *Solanaceae* production. This study highlighted the strain LNPV24.25, which was isolated from a diseased tomato and belong to the phylotype IIB-4NPB that gather highly aggressive and virulent emerging strains. This indicates, from our knowledge, the first report of an emerging strain in France.

These findings showed that pathogenicity traits of genetically identified strains still need to be understood, especially in the perspective of post-genomics comparative analysis to understand bacterial speciation in the *R. solanacearum* species complex.

Keywords:
Ralstonia solanacearum, bacterial wilt, pathogenicity, brown rot, Moko disease